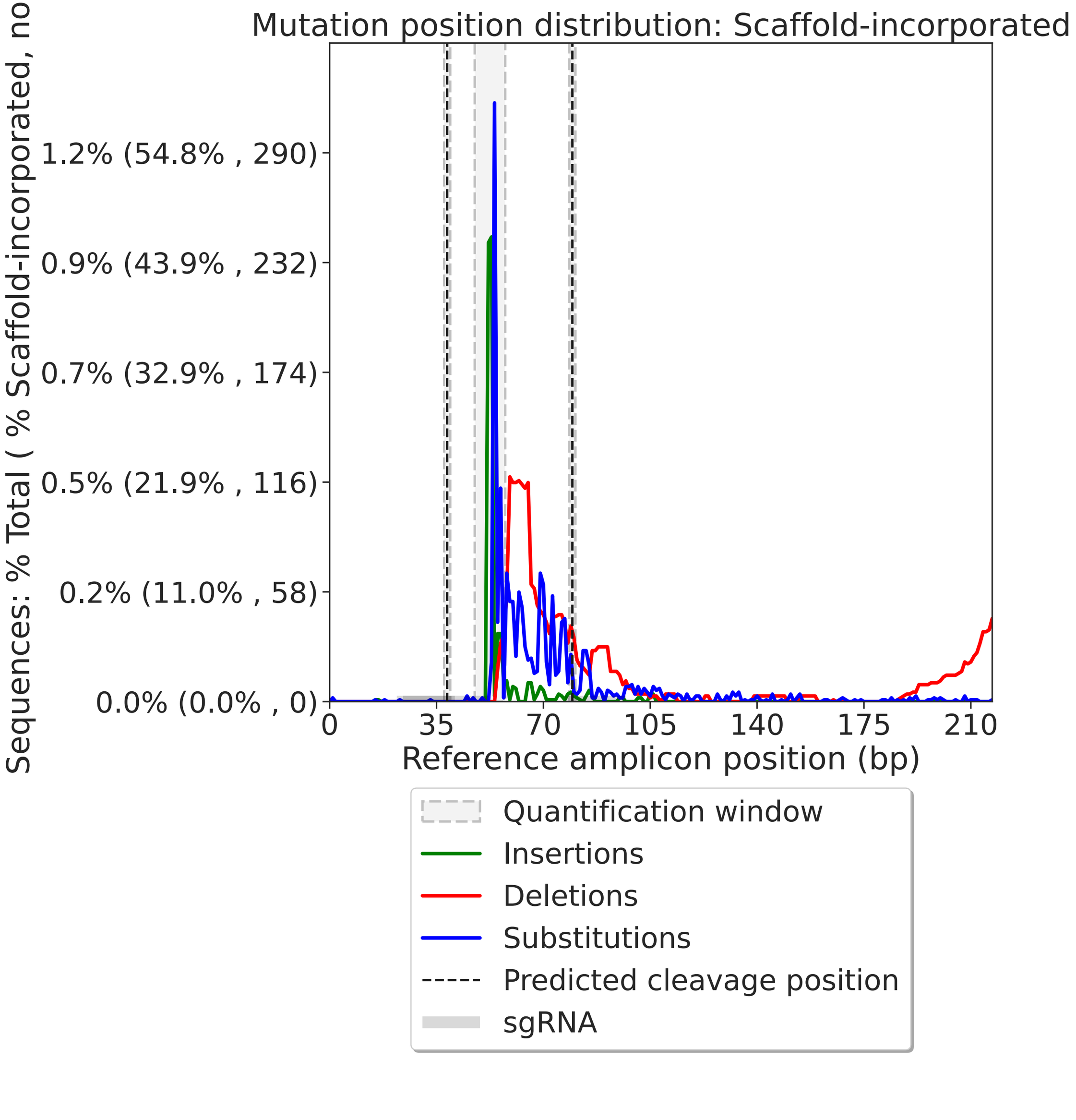
Mutation position distribution: Scaffold-incorporated
Sequences: % Total (% Scaffold-incorporated, no.)
1.2% (54.8% , 290)
0.9% (43.9% , 232)
0.7% (32.9% , 174)
0.5% (21.9% , 116)
0.2% (11.0% , 58)
0.0% (0.0% , 0)
0
35
70
105
140
175
210
Reference amplicon position (bp)
Quantification window
Insertions
Deletions
Substitutions
Predicted cleavage position
sgRNA